

SEQUENCE LISTING

<110> Novo Nordisk A/S

<120> TRANSGENIC PLANT EXPRESSING MALTOGENIC ALPHA-AMYLASE

<130> 5753A

<140>

<141>

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2160

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)..(2160)

<220>

<221> mat_peptide

<222> (100)..(2157)

<400> 1

atg aaa aag aaa acg ctt tct tta ttt gtg gga ctg atg ctc ctc atc	48
Met Lys Lys Lys Thr Leu Ser Leu Phe Val Gly Leu Met Leu Leu Ile	
-30 -25 -20	
ggt ctt ctg ttc agc ggt tct ctt ccg tac aat cca aac gcc gct gaa	96
Gly Leu Leu Phe Ser Gly Ser Leu Pro Tyr Asn Pro Asn Ala Ala Glu	
-15 -10 -5	
gcc agc agt tcc gca agc gtc aaa ggg gac gtg att tac cag att atc	144
Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile	
-1 1 5 10 15	
att gac cgg ttt tac gat ggg gac acg acg aac aac aat cct gcc aaa	192
Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys	
20 25 30	
agt tat gga ctt tac gat ccg acc aaa tcg aag tgg aaa atg tat tgg	240
Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp	
35 40 45	

ggc ggg gat ctg gag ggg gtt cgt caa aaa ctt cct tat ctt aaa cag 288
 Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
 50 55 60

ctg ggc gta acg aca atc tgg ttg tcc ccg gtt ttg gac aat ctg gat 336
 Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
 65 70 75

aca ctg gcg ggc acc gat aac acg ggc tat cac gga tac tgg acg cgc 384
 Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
 80 85 90 95

gat ttt aaa cag att gag gaa cat ttc ggg aat tgg acc aca ttt gac 432
 Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
 100 105 110

acg ttg gtc aat gat gct cac caa aac gga atc aag gtg att gtc gac 480
 Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
 115 120 125

ttt gtg ccc aat cat tcg act cct ttt aag gca aac gat tcc acc ttt 528
 Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
 130 135 140

gcg gaa ggc ggc gcc ctc tac aac aat gga acc tat atg ggc aat tat 576
 Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
 145 150 155

ttt gat gac gca aca aaa ggg tac ttc cac cat aat ggg gac atc agc 624
 Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
 160 165 170 175

aac tgg gac gac cgg tac gag gcg caa tgg aaa aac ttc acg gat cca 672
 Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
 180 185 190

gcc ggt ttc tcg ctt gcc gat ttg tcg cag gaa aat ggc acg att gct 720
 Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
 195 200 205

caa tac ctg acc gat gcg gcg gtt caa ttg gta gca cat gga gcg gat 768
 Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
 210 215 220

ggt ttg cgg att gat gcg gtg aag cat ttt aat tcg ggg ttc tcc aaa 816
 Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
 225 230 235

tcg ttg gcc gat aaa ctg tac caa aag aaa gac att ttc ctg gtg ggg 864
 Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly
 240 245 250 255

gaa tgg tac gga gat gac ccc gga aca gcc aat cat ctg gaa aag gtc 912
 Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val
 260 265 270

cgg tac gcc aac aac agc ggt gtc aat gtg ctg gat ttt gat ctc aac 960
 Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn
 275 280 285

acg gtg att cga aat gtg ttc ggc aca ttt acg caa acg atg tac gat 1008
 Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp
 290 295 300

ctt aac aat atg gtg aac caa acg ggg aac gag tac aaa tac aaa gaa 1056
 Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu
 305 310 315

aat cta atc aca ttt atc gat aac cat gat atg tca aga ttt ctt tcg 1104
 Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser
 320 325 330 335

gta aat tcg aac aag gcg aat ttg cac cag gcg ctt gct ttc att ctc 1152
 Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu
 340 345 350

act tcg cgg ggt acg ccc tcc atc tat tat gga acc gaa caa tac atg 1200
 Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met
 355 360 365

gca ggc ggc aat gac ccg tac aac cgg ggg atg atg ccg gcg ttt gat 1248
 Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp
 370 375 380

acg aca acc acc gcc ttt aaa gag gtg tca act ctg gcg ggg ttg cgc 1296
 Thr Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg
 385 390 395

agg aac aat gcg gcg atc cag tac ggc acc acc acc cag cgt tgg atc 1344
 Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile
 400 405 410 415

aac aat gat gtt tac att tat gaa cgg aaa ttt ttc aac gat gtc gtg 1392
 Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val
 420 425 430

ttg gtg gcc atc aat cga aac acg caa tcc tcc tat tcg att tcc ggt 1440
 Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly
 435 440 445

ttg cag acg gcc ttg cca aat ggc agc tat gcg gat tat ctg tca ggg 1488
 Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly
 450 455 460

ctg ttg ggg ggg aac ggg att tcc gtt tcc aat gga agt gtc gct tcg 1536
 Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser
 465 470 475

ttc acg ctt gcg cct gga gcc gtg tct gtt tgg cag tac agc aca tcc 1584
 Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser
 480 485 490 495

gct tca gcg ccg caa atc gga tcg gtt gct cca aat atg ggg att ccg 1632
 Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro
 500 505 510

ggt aat gtg gtc acg atc gac ggg aaa ggt ttt ggg acg acg cag gga 1680
 Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly
 515 520 525

acc gtg aca ttt ggc gga gtg aca gcg act gtg aaa tcc tgg aca tcc 1728
 Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser
 530 535 540

aat cgg att gaa gtg tac gtt ccc aac atg gcc gcc ggg ctg acc gat 1776
 Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp
 545 550 555

gtg aaa gtc acc gcg ggt gga gtt tcc agc aat ctg tat tct tac aat 1824
 Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn
 560 565 570 575

att ttg agt gga acg cag aca tcg gtt gtg ttt act gtg aaa agt gcg 1872
 Ile Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala
 580 585 590

cct ccg acc aac ctg ggg gat aag att tac ctg acg ggc aac ata ccg 1920
 Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro
 595 600 605

gaa ttg ggg aat tgg agc acg gat acg agc gga gcc gtt aac aat gcg 1968
 Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala
 610 615 620

caa ggg ccc ctg ctc gcg ccc aat tat ccg gat tgg ttt tat gta ttc 2016
 Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
 625 630 635

agc gtt cca gca gga aag acg att caa ttc aag ttc ttc atc aag cgt 2064
 Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg
 640 645 650 655

gcg gat gga acg att caa tgg gag aat ggt tgc aac cac gtg gcc aca 2112
 Ala Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr
 660 665 670

act ccc acg ggt gca acc ggt aac att act gtt acg tgg caa aac tag 2160
 Thr Pro Thr Gly Ala Thr Gly Asn Ile Thr Val Thr Trp Gln Asn
 675 680 685

<210> 2

<211> 719

<212> PRT

<213> Bacillus sp.

<400> 2

Met Lys Lys Lys Thr Leu Ser Leu Phe Val Gly Leu Met Leu Leu Ile
 1 5 10 15

Gly Leu Leu Phe Ser Gly Ser Leu Pro Tyr Asn Pro Asn Ala Ala Glu
 20 25 30

Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
 35 40 45

Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
 50 55 60

Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
 65 70 75 80

Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
 85 90 95

Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
 100 105 110

Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
 115 120 125

Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
 130 135 140
 Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
 145 150 155 160
 Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
 165 170 175
 Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
 180 185 190
 Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
 195 200 205
 Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
 210 215 220
 Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
 225 230 235 240
 Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
 245 250 255
 Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
 260 265 270
 Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly
 275 280 285
 Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val
 290 295 300
 Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn
 305 310 315 320
 Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp
 325 330 335
 Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu
 340 345 350
 Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser
 355 360 365
 Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu
 370 375 380

Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met
 385 390 395 400
 Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp
 405 410 415
 Thr Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg
 420 425 430
 Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile
 435 440 445
 Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val
 450 455 460
 Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly
 465 470 475 480
 Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly
 485 490 495
 Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser
 500 505 510
 Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser
 515 520 525
 Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro
 530 535 540
 Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly
 545 550 555 560
 Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser
 565 570 575
 Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp
 580 585 590
 Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn
 595 600 605
 Ile Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala
 610 615 620
 Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro
 625 630 635 640

Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala
 645 650 655

Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
 660 665 670

Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg
 675 680 685

Ala Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr
 690 695 700

Thr Pro Thr Gly Ala Thr Gly Asn Ile Thr Val Thr Trp Gln Asn
 705 710 715

<210> 3

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FNP110

<400> 3

tcccccgga tgagcagttc cgcaagcgtc aaa

33

<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:RNP110

<400> 4

cgatgagctc ctagttttgc cacgt

25